

IN THE CLAIMS:

Please amend claims 3-7 and 14-15 as follows:

1-2. (Cancelled)

3. (Currently Amended) A method for displaying gene expression data in comparing gene expression levels of a plurality of common genes for different samples A, B, C, comprising:

calculating a first ratio $[[b/a1]] \ b/a$ of a gene expression level b of each of said common genes for the $[[a]]$ Sample B with respect to a gene expression level $[[a1]]a$ of said gene for the $[[a]]$ Sample A for each of a plurality of genes in a first experiment;

calculating a second ratio $[[c/a2]] \ c/A$ of a gene expression level c of said gene for the $[[a]]$ Sample C with respect to a gene expression level $[[a2]]A$ of said gene for the Sample A for said each of a plurality of genes in a second experiment;

obtaining a ~~mediated~~ dataset of gene expression levels for the Samples B, C, A expressed as $(b/a, c/A, 1)$ ~~$(b/a1, c/a2, 1)$~~ for said each of a plurality of genes;

calculating a first magnitude r of said dataset expressed as $r = \sqrt{\{(b/a)^2 + (c/A)^2 + 1\}}$ ~~$r = \sqrt{\{(b/a1)^2 + (c/a2)^2 + 1\}}$~~ ; and

displaying a mark of a first product of the first ratio and $[[1/r]] \ K/r$, a second product of the second ratio and the $[[1/r]] \ K/r$, and the $[[1/r]] \ K/r$ on a coordinate position with respect to x-, y- and z-axes on a surface of a sphere for said each of a plurality of genes, K being a radius of the sphere, to thereby compare gene expression levels of the plurality of common genes for the samples A, B, C.

4. (Currently Amended) A method for displaying gene expression data according to claim 3, further comprising: calculating a second magnitude R of said dataset expressed as $R = \sqrt{\{b^2 + c^2 + (a + A)^2\}}$ ~~$R = \sqrt{\{b^2 + c^2 + (a1 + a2)^2\}}$~~ displaying a mark of a third product of the first ratio and R/r , a fourth product of the second ratio and the R/r , and the R/r on a coordinate positions with respect to x-, y- and z-axes for said each of a plurality of common genes.

5. (Currently Amended) A method for displaying gene expression data according to claim 3, further comprising: performing a clustering analysis on the displayed marks for said plurality of common genes on the sphere; and marking at least one gene group obtained by the clustering analysis as a region on the sphere.
6. (Currently Amended) A method for displaying gene expression data according to claim 4, further comprising: performing a clustering analysis on the displayed magnitude coordinate positions inside the sphere for said plurality of common genes; and marking at least one gene group obtained by the clustering analysis as a region inside the sphere.
7. (Currently Amended) A method for displaying gene expression data according to claim 3, wherein the expression level data is data in a time series, which is displayed based on respective time points for said each of a plurality of common genes in conjunction with a direction of changes of the coordinate positions with time in the displaying step.
8. (Previously Presented) A method for displaying gene expression data according to claim 5, wherein the expression level data is data in a time series, and said region is displayed based on respective time points in conjunction with a direction of changes of said region with time in the displaying step.
- 9-13. (Cancelled)
14. (Currently Amended) A method for displaying gene expression data according to claim 4, wherein the expression level data is data in a time series, which is displayed based on respective time points for said each of a plurality of common genes in conjunction with a direction of changes of the coordinate positions with time in the displaying step.
15. (Currently Amended) A method for displaying gene expression data according to claim 5, wherein the expression level data is data in a time series, which is displayed based on respective time points for said each of a plurality of common genes in

conjunction with a direction of changes of the coordinate positions with time in the displaying step.

16. (Original) A method for displaying gene expression data according to claim 6, wherein the expression level data is data in a time series, and said region is displayed based on respective time points in conjunction with a direction of changes of said region with time in the displaying step.
17. (Cancelled)